

CLAIMS

What is claimed is:

1. A method for the directed integration of an expressible DNA fragment lacking a selectable marker into a bacterial chromosome comprising:
 - a) providing at least one first recombination element having the general structure in the 5' to 3' direction:
5'-RR1-RS-SM-RS-RR2-3'; wherein
 - (i) RR1 is a first recombination region of about 10 to 50 bases;
 - (ii) RS is a recombination site responsive to a site-specific recombinase;
 - (iii) SM is a DNA fragment encoding a selectable marker; and
 - (iv) RR2 is a second recombination region of about 10 to 50 bases;
 - b) providing at least one second recombination element having the general structure in a 5' to 3' direction:
X-RR3; wherein
 - (i) X is an expressible DNA fragment having homology to the second recombination region; and
 - (ii) RR3 is a third recombination of about 10-50 bases;
 - c) providing a recombination proficient bacterial host harboring a λ-Red recombinase system, having a bacterial chromosome comprising:
 - (i) a first chromosomal region having homology to said first recombination region;
 - (ii) a second chromosomal region having homology to said third recombination region;
 - d) transforming said recombination proficient host with the first and second recombination elements, wherein both elements are integrated into the bacterial chromosome between the first and second chromosomal regions forming a construct having the general structure in the 5' to 3' direction;
5'-RR1-RS-SM-RS-RR2-X-RR3;
 - e) selecting and isolating transformed hosts having the construct of (d) on the basis of the selectable marker;

- 5 f) expressing a site-specific recombinase in the isolated hosts of (e) wherein the selectable marker is excised from the chromosome and whereby the expressible DNA fragment is inserted into the bacterial chromosome, lacking the selectable marker.

2. A method for the directed integration of an expressible DNA fragment lacking a selectable marker into a bacterial chromosome comprising:

- 10 a) providing at least one first recombination element having the general structure in the 5' to 3' direction:
5'-RR1-RS-SM-RS-Y-RR2-3'; wherein
15 (i) RR1 is a first recombination region of about 10 to 50 bases;
 (ii) RS is a recombination site responsive to a site-specific recombinase;
 (iii) SM is a DNA fragment encoding a selectable marker;
 (iv) Y is a first expressible DNA fragment; and
 (v) RR2 is a second recombination region of about 10 to 20 50 bases;
- 20 b) providing at least one second recombination element having the general structure in a 5' to 3' direction:
5'-X-RR3-3'; wherein
25 (i) X is a second expressible DNA fragment having homology to the second recombination region; and
 (ii) RR3 is a third recombination of about 10-50 bases;
- 30 c) providing a recombination proficient bacterial host harboring a λ -Red recombinase system, and having a bacterial chromosome comprising:
 (i) a first chromosomal region having homology to said first recombination region;
 (ii) a second chromosomal region having homology to said third recombination region;
- 35 d) transforming said recombination proficient host with the first and second recombination elements, wherein both elements are integrated into the bacterial chromosome between the first and second chromosomal regions

- forming a construct having the general structure in the 5'
to 3' direction;
5'-RR1-RS-SM-RS-Y-RR2-X-RR3;
- 5 e) selecting and isolating transformed hosts having the
construct of (d) on the basis of the selectable marker;
f) expressing a site-specific recombinase in the isolated
hosts of (e) wherein the selectable marker is excised from
the chromosome and whereby the first and second
expressible DNA fragments are inserted into the bacterial
chromosome, lacking the selectable marker.
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3. A method according to either one of Claims 1 or 2 wherein
either the first or second the expressible DNA fragment is selected from
the group consisting of regulatory elements, promoters, genes, coding
sequences, and open reading frames.
- 15 4. A method according to either one of Claims 1 or 2 wherein the
site-specific recombinase is expressed by a gene residing on a plasmid.
5. A method according to either one of Claims 1 or 2 wherein said
first chromosomal region is upstream of a bacterial promoter.
- 20 6. A method according to either one of Claims 1 or 2 wherein said
first chromosomal region is upstream of an inter-operon chromosomal
integration site.
7. A method according to Claim 3 wherein said expressible DNA
fragment is a promoter selected from the group consisting of bacterial and
phage promoters.
- 25 8. A method according to Claim 7 wherein said promoter
comprises positive and negative regulatory sites for control of a regulatory
circuit.
9. A method according to Claim 8 wherein said regulatory region
comprises a *lac* operator site.
- 30 10. A method according to Claim 7 wherein said promoter is
selected from the group consisting of the phage T5 promoter, the phage
T7 promoter, and the *lac* promoter.
- 35 11. A method according to either one of Claims 1 or 2 wherein said
selectable marker is selected from the group consisting of antibiotic
resistance markers, enzymatic markers and amino acid biosynthesis
enzymes.
12. A method according to either one of Claims 1 or 2 wherein said
recombination proficient host harboring a λ -Red recombinase system is

selected from the group consisting of *Escherichia*, *Salmonella*, *Acinetobacter*, *Methylomonas*, *Bacillus*, and *Pseudomonas*.

13. A method according to either one of Claims 1 or 2 wherein said recombination sites are selected from the group consisting of *lox*, *frt*, *dif*,
5 and *att*.
14. A method according to Claim 13 wherein said site-specific recombinase is selected from the group consisting of Cre, Flp, Xer, and Int.
- 10 15. A method according to either one of Claims 1 or 2 wherein said recombination elements are generated by PCR.
16. A method according to either one of Claims 1 or 2 wherein said recombination elements are from about 25 bases to about 4000 bases.
17. A method for the integration of a foreign promoter in place of a bacterial chromosomal promoter in a recombination proficient host cell
15 comprising:
- a) providing at least one first recombination element having the general structure in the 5' to 3' direction:
5'-RR1-RS-SM-RS-RR2-3'; wherein
 - (i) RR1 is a first recombination region of about 10 to 50 bases;
 - (ii) RS is a recombination site responsive to a site-specific recombinase;
 - (iii) SM is a DNA fragment encoding a selectable marker; and
 - (iv) RR2 is a second recombination region of about 10 to 50 bases;
 - b) providing at least one second recombination element having the general structure in a 5' to 3' direction:
5'-FP-RR3-3'; wherein
 - (i) FP is a promoter foreign to the recombination proficient host cell having homology to the second recombination region; and
 - (ii) RR3 is a third recombination of about 10-50 bases;
 - c) providing a recombination proficient bacterial host harboring a λ -Red recombinase system, having a bacterial chromosome comprising:

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- (i) a first chromosomal region upstream of a bacterial promoter having homology to said first recombination region;
 - (ii) a second chromosomal region, downstream of said bacterial promoter having homology to said third recombination region;
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- d) transforming said recombination proficient host with the first and second recombination elements, wherein both elements are integrated into the bacterial chromosome between the first and second chromosomal regions forming a construct having the general structure in the 5' to 3' direction:
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- 5'-RR1-RS-SM-RS-RR2-FP-RR3;
 - e) selecting and isolating transformed hosts having the construct of (d) on the basis of the selectable marker;
 - f) expressing a site-specific recombinase in the isolated hosts of (e) wherein the selectable marker is excised from the chromosome and whereby the foreign promoter is inserted into the bacterial chromosome in place of the bacterial promoter.
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18. A method for the integration of an unlinked foreign promoter and foreign open reading frame into a bacterial chromosome in a recombination proficient host cell comprising:

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- a) providing at least one first recombination element having the general structure in the 5' to 3' direction:
5'-RR1-RS-SM-RS-FP-RR2-3'; wherein
 - (i) RR1 is a first recombination region of about 10 to 50 bases;
 - (ii) RS is a recombination site responsive to a site-specific recombinase;
 - (iii) SM is a DNA fragment encoding a selectable marker;
 - (iv) FP is a promoter foreign to the recombination proficient host cell; and
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- (iv) RR2 is a second recombination region of about 10 to 50 bases;
 - b) providing at least one second recombination element having the general structure in a 5' to 3' direction:
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5'-FO-RR3-3'; wherein

- (i) FO is an open reading frame foreign to the recombination proficient host cell having homology to the second recombination region; and
 - 5 (ii) RR3 is a third recombination of about 10-50 bases;
 - c) providing a recombination proficient bacterial host harboring a λ -Red recombinase system, having a bacterial chromosome comprising:
 - (i) a first chromosomal region upstream of a bacterial intra-operon chromosomal integration site having homology to said first recombination region;
 - 10 (ii) a second chromosomal region, downstream of said bacterial intra-operon chromosomal integration site having homology to said third recombination region;
 - 15 d) transforming said recombination proficient host with the first and second recombination elements, wherein both elements are integrated into the bacterial chromosome between the first and second chromosomal regions forming a construct having the general structure in the 5' to 3' direction;
 - 20 5'-RR1-RS-SM-RS-FP-RR2-FO-RR3;
 - e) selecting and isolating transformed hosts having the construct of (d) on the basis of the selectable marker;
 - f) expressing a site-specific recombinase in the isolated
- 25 hosts of (e) wherein the selectable marker is excised from the chromosome and whereby the foreign promoter and foreign open reading frame are inserted into the bacterial chromosome.

19. A method for the integration of a foreign gene comprising a regulatory region and foreign open reading frame into a bacterial chromosome in a recombination proficient host cell comprising:

- a) providing at least one first recombination element having the general structure in the 5' to 3' direction:

5'-RR1-RS-SM-RS-FG-RR2-3'; wherein

- (i) RR1 is a first recombination region of about 10 to 50 bases;
- (ii) RS is a recombination site responsive to a site-specific recombinase;

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- (iii) SM is a DNA fragment encoding a selectable marker;
 - (iv) FG is a gene comprising a regulatory region, foreign to the recombination proficient host cell; and
 - (iv) RR2 is a second recombination region of about 10 to 50 bases;
- b) providing at least one second recombination element having the general structure in a 5' to 3' direction:
5'-FO-RR3-3'; wherein
- 10 (i) FO is an open reading frame foreign to the recombination proficient host cell having homology to the second recombination region; and
 - (ii) RR3 is a third recombination of about 10-50 bases;
- c) providing a recombination proficient bacterial host harboring a λ -Red recombinase system, having a bacterial chromosome comprising:
- 15 (i) a first chromosomal region upstream of a bacterial intra-operon chromosomal integration site having homology to said first recombination region;
 - (ii) a second chromosomal region, downstream of said bacterial intra-operon chromosomal integration site having homology to said third recombination region;
- d) transforming said recombination proficient host with the first and second recombination elements, wherein both elements are integrated into the bacterial chromosome between the first and second chromosomal regions forming a construct having the general structure in the 5' to 3' direction;
20 5'-RR1-RS-SM-RS-FG-RR2-FO-RR3;
- e) selecting and isolating transformed hosts having the construct of (d) on the basis of the selectable marker;
- f) expressing a site-specific recombinase in the isolated hosts of (e) wherein the selectable marker is excised from the chromosome and whereby the foreign promoter and 25 foreign open reading frame are inserted into the bacterial chromosome.
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20. A method according to any one of Claims 17-19 wherein the site-specific recombinase is expressed by a gene residing on a plasmid.

21. A method according to Claim 17 wherein said promoter is selected from the group consisting of bacterial and phage promoters.
22. A method according to Claim 21 wherein said promoter comprises positive and negative regulatory sites for control of regulatory circuit.
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23. A method according to Claim 22 wherein said regulatory region comprises a *lac* operator site.
24. A method according to Claim 21 wherein said promoter is selected from the group consisting of the phage *T5* promoter, the phage *T7* promoter, and the *lac* promoter.
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25. A method according to any one of Claims 17-19 wherein said recombination proficient host harboring a λ -Red recombinase system is selected from the group consisting of *Escherichia*, *Salmonella*, *Acinetobacter*, *Methyloimonas*, *Bacillus*, and *Pseudomonas*.
- 15 26. A method according to any one of Claims 17-19 wherein said recombination sites are selected from the group consisting of *lox*, *frt*, *dif*, and *att*.
- 20 27. A method according to Claim 26 wherein said site-specific recombinase is selected from the group consisting of *Cre*, *Flp*, *Xer*, and *Int*.
28. A method according to any one of Claims 17-19 wherein said recombination elements are generated by PCR.
29. A method according to either one of Claims 17-19 wherein said recombination elements are from about 25 bases to about 4000 bases.
- 25 30. A method according to any of Claims 1,2, 17-19 wherein steps (d) – (f) are repeated one or more times.